

Figure 1A

1	ATGACAACTCTGTTCTGCAACCCTCTCCCTCTCTCTGGACCCGCCAGGGCAG	60
1	M T T L V P A T L S F L L L W T L P G Q	20
61	GTCCTCCTCAGGGTGGCCTTGGCAAAAGAGGAAGTCAAATCTGGAACCAAGGGTCCAG	120
21	V L L R V A L A K E E V K S G T K G S Q	40
121	CCCATGTCCCCCTCTGATTCCTAGACAAACTATGGGCGAACATCTGGATATGATGCC	180
41	P M S P S D F L D K L M G R T S G Y D A	60
181	AGGATTGGGCCAATTAAAGGCCACCGTGAAACGTGACCTGCAACATCTTCATCAAC	240
61	R I R P N F K G P P V N V T C N I F I N	80
241	AGTTTCAGCTCCGTACCAAGACCACAATGGACTACCGGGTGAATGTCTTCTGCGGCAA	300
81	S F S S V T K T T M D Y R V N V F L R Q	100
301	CAGTGGAAATGACCCACGCCTGTCCTACCGAGAATATCCTGATGACTCTGGACCTCGAT	360
101	Q W N D P R L S Y R E Y P D D S L D L D	120
361	CCCTCCATGCTGGACTCTATCTGGAAGCCAGACCTCTTCTTGCTAATGAGAAAGGGCC	420
121	P S M L D S I W K P D L F F A N E K G A	140
421	AACTTCCATGAGGTGACCACGGACAACAAGTTACTGCGCATCTTCAAGAATGGGAATGTG	480
141	N F H E V T T D N K L L R I F K N G N V	160
481	CTGTACAGCATCAGGCTGACCCCTATTTGTCCTGCCTGATGGACCTCAAGAACTTCCCC	540
161	L Y S I R L T L I L S C L M D L K N F P	180
541	ATGGACATCCAGACCTGCACGATGCAGCTTGAGAGCTTGGCTACACCATGAAAGACCTC	600
181	M D I Q T C T M Q L E S <u>F G Y</u> T M K D L	200
601	GTGTTGAGTGGCTGGAAGATGCTCCTGCTGTCCAAGTGGCTGAGGGCTGACTCTGCC	660
201	V F E W L E D A P A V Q V A E G L T L P	220
661	CAGTTTATCTGCGGGATGAGAAGGATCTAGGCTGTTGACCAAGCACTACAACACAGGG	720
221	Q F I L R D E K D L G C C T <u>K H Y N T</u> G	240
721	AAATTCACCTGCATCGAGGTAAAGTTCACCTGGAACGGCAGATGGCTACTATCTGATT	780
241	K F T C I E V K F H L E R Q <u>M G Y Y L I</u>	260
781	CAGATGTACATCCCCAGCCTACTCATCGTCATCCTGTCCTGGGTCTCCTCTGGATCAAC	840
261	<u>Q M Y I P S L L I V I L S W V S F W I N</u>	280
841	ATGGATGCTGCCCTGCCCCTGGGCTGGGCATCACCAACCGTGCTCACCATGACCACC	900
281	<u>M D A A P A R V G L G I T T V L T M T T</u>	300

Figure 1B

901	CAGAGCTCTGGCTCCGGGCCTTTGCCTAAGGTGTCCTACGTGAAGGCAATCGACATC	960
301	<u>Q S S G S R A S L P K V S Y V K A I D I</u>	320
961	TGGATGGCTGTGTCTGCTCTTGTGTTGCTGCCTGCTGGAGTATGCTGCCATAAAT	1020
321	<u>W M A V C L L F V F A A L L E Y A A I N</u>	340
1021	TTTGTTCCTCGTCAGCATAAAGAATTACGACTTCGAAGAAGGCAGAGGCGCCAACGC	1080
341	<u>F V S R Q H K E F I R L R R R Q R R Q R</u>	360
1081	TTGGAGGAAGATATCATCCAAGAAAGTCGTTCTATTCCGTGGCTATGGCTGGCCAC	1140
361	L E E D I I Q E S R F Y F R G Y G L G H	380
1141	TGCCTGCAGGCAAGAGATGGAGGTCCAATGGAAGGTTCTGGCATTATAGTCCCCAACCT	1200
381	C L Q A R D G G P M E G S G I Y S P Q P	400
1201	CCAGCCCCCTTCTAAGGGAAGGAGAAACCACGCGGAAACTCTACGTGGACTGAGCCAAG	1260
401	P A P L L R E G E T T R K L Y V D	417
1261	AGAATTGACACCATCTCCGGCTGTCTCCCTTCACTTCCCTCATCTCAATATCTTC	1320
1321	TACTGGTTGTCTATAAGTGCACGGTCAGAAGATATCCACCGAGCTGTGAATAGGG	1380
1381	TGGGAGCTATAGAGTCCTGCTGGCCTCCTGCTTCCTGGTGGCTTCTCCCT	1440
1441	AGTTAGACTCCATTAGGGTTGGACAGTTCCCTGATCTCCACTCAGAACTCAAC	1500
1501	TACCAAGTCCAAAGCTATGTGGCCTATATTGCATGGTCCAATGGTGGCTGTACTTATA	1560
1561	AAGATGGCTTATCTACCCCTAGTCATATTTCTCCATACTTCCCATTCTCATGAGACT	1620
1621	AAGGTTGGCCACATTCCCTGGGCCAGGATGACCTCTGCCCTGCTGGAGCCTCCGT	1680
1681	TTTCCAATACTCCAGTGGAGAGTATTCAAGAACACTGCTGCTAGATTCTGGCATTGTCAT	1740
1741	CTTAATCTGCACCACTTCTCCCCCTGCCACCTCCCACCCAGAGCCTGGCCATTACTCTGT	1800
1801	CCTCTGTCCCTCTGCTGCAGATTCAAATGGTGAGTTCTCCTATCCACAAAGTGCTGCC	1860
1861	TGTGGGGCCTAGTCAGGTTCTTGAAGTGAGAGGAAGGCAAAGCCGCAAGTCCCCACC	1920
1921	TCTCGAGAGGGTTGGAACAGTCATAGGCTGCACTGGCTAGCGACTATATGGCCCAACAG	1980

**Figure 1C**

1981 AGAGGTGTTCAAGTCTCTGGGAAGCCCCACACTTGTCTTCATCCCTTCCTATTGCG 2040  
2041 CTTGTCTGCTCTTCCTGTTCACTGAGATACTCCTCTGTCTGTCTCTAGTTGAGGA 2100  
2101 GAGCGTTCTGAGCTGACCAGGGTAGCTGGTCAGAAATTACTGTCAGAATTGGGGCAGAG 2160  
2161 ACTTTGGGTTCTCAAAAAGACTAACCTCCAGATCCACCTGAACATTCTGGTCTCAGAAA 2220  
2221 TATTGTTCCCGTCCCTAATTAACCTAGCATGGTGGCAGGATCTGTTGGACAGCTGGGAG 2280  
2281 TGTAAAAAAAGAAAAACTTGTCTTTAAGAAACTTACTTATGATGCTAGAAAACCTT 2340  
2341 TGAGAAAAGTGAGATCCAAGGTAGTGGAACCCAGGAGGAGTAGAATAGAGAAACTATTCT 2400  
2401 CAGAGTGTCTTGTGGCTGGCTTCATTTGTTCTTCTCACCAAAGTCTATT 2460  
2461 TCCAGGGCCCTCATTCCAACCTGGTCTTCACCTCCTTGGTGTGCAAATAAGGTG 2520  
2521 CCGCTGCAACCTGTTAAGGATAAAAAAAAAAAAAAAAAAAAAA 2565

Figure 2A

1	ATGACAAC	CTTGT	TCCTG	CAAC	CCCTCT	CCCTCT	CTCTG	GGAC	CCAG	GGCAG	60													
1	M	T	T	L	V	P	A	T	L	S	F	L	L	L	W	T	L	P	G	Q	20			
61	GTC	CCTC	AGGGT	GGCCT	TGG	AAAAG	AGGAAG	TCAA	ATCTG	GAAC	CAAGGGT	CCCAG	120											
21	V	L	L	R	V	A	L	A	K	E	E	V	K	S	G	T	K	G	S	Q	40			
121	CCC	ATGT	CCCC	CTG	AT	TC	TA	GA	CAAA	ACTT	ATGGG	CGAAC	ATCTG	GAAT	GAT	ATG	GCC	180						
41	P	M	S	P	S	D	F	L	D	K	L	M	G	R	T	S	G	Y	D	A	60			
181	AGG	ATT	CGGCC	CA	TTT	AAAGG	CCCAC	CCGT	GAAC	GTGAC	CTG	CAAC	ATCT	CATCAAC							240			
61	R	I	R	P	N	F	K	G	P	P	V	N	V	T	C	N	I	F	I	N	80			
241	AGTT	TCAG	CTCG	TCAC	CAAG	ACCAC	AA	ATGG	ACTAC	CGGGT	GAAT	GTCTT	CTTGC	GGCAA							300			
81	S	F	S	S	V	T	K	T	T	M	D	Y	R	V	N	V	F	L	R	Q	100			
301	CAG	TGGA	ATG	ACCC	AC	GC	CT	GT	CC	TAC	CGAGA	ATAT	CCTG	ATG	ACT	CT	GGAC	CTCG	AT		360			
101	Q	W	N	D	P	R	L	S	Y	R	E	Y	P	D	D	S	L	D	L	D	120			
361	CC	CT	CC	CATG	CTGG	ACTCT	ATCTG	GAAG	CCAGAC	CTCTT	CTTG	CTAAT	GAGAA	AGGGC							420			
121	P	S	M	L	D	S	I	W	K	P	D	L	F	F	A	N	E	K	G	A	140			
421	AACT	TCC	CATG	AGGT	GACC	ACGG	ACA	AA	AGTT	ACTG	CGC	CATCTT	CAAGA	ATGG	AA	GTG					480			
141	N	F	H	E	V	T	T	D	N	K	L	L	R	I	F	K	N	G	N	V	160			
481	CTG	TAC	AGC	CAT	CAGG	CTG	ACCC	TC	ATTT	GT	CC	TG	CTG	ATGG	ACCT	CAAGA	ACT	CCCC			540			
161	L	Y	S	I	R	L	T	L	I	L	S	C	L	M	D	L	K	N	F	P	180			
541	ATGG	ACAT	CC	CAG	ACGT	GCAC	GTG	ACG	ATG	GCAG	CTG	AG	AG	CT	CAT	CC	ATA	CT	GCAG	CCCT	TG	600		
181	M	D	I	Q	T	C	T	M	Q	L	E	S	S	S	I	L	C	S	P	L	200			
601	CC	AT	CT	GT	CA	TT	CAG	TTGG	CT	AC	ACC	AT	GAA	AGAC	CT	CGT	TTG	GAG	GTG	CTGGAA		660		
201	P	S	L	S	L	S	V	<b>S</b>	<b>Y</b>	T	M	K	D	L	V	F	E	W	L	E	220			
661	GAT	GCT	CCTG	GCTG	CCA	AGT	GGCT	GAG	GGCT	GACT	CT	GCC	CC	AG	TT	AT	CTT	GC	GGG	AT		720		
221	D	A	P	A	V	Q	V	A	E	G	L	T	L	P	Q	F	I	L	R	D	240			
721	GAGA	AGG	ATC	AGG	CTG	TG	TG	TG	ACCA	AGC	ACT	ACA	AC	AGG	AA	AT	TC	AC	CTG	CAG		780		
241	E	K	D	L	G	C	C	T	<b>K</b>	<b>H</b>	<b>Y</b>	<b>X</b>	<b>Y</b>	<b>G</b>	<b>K</b>	<b>F</b>	<b>T</b>	<b>C</b>	<b>I</b>	<b>E</b>	260			
781	GTAA	AG	TT	CAC	CTG	GAAC	GGC	AG	AT	GGG	CT	ACT	AT	CTG	ATT	CA	AG	AT	GT	AC	AT	CCCC	AGC	840
261	V	K	F	H	L	E	R	Q	<u>M</u>	<u>G</u>	<u>Y</u>	<u>Y</u>	<u>L</u>	<u>I</u>	<u>Q</u>	<u>M</u>	<u>Y</u>	<u>I</u>	<u>P</u>	<u>S</u>	280			
841	CTACT	CAT	CGT	CAT	CCTG	TG	CTGG	CT	CC	TT	CTG	GG	AT	CA	AC	AT	GG	AT	GT	GC	CC	CTG	CC	900
281	<u>L</u>	<u>L</u>	<u>I</u>	<u>V</u>	<u>I</u>	<u>L</u>	<u>S</u>	<u>W</u>	<u>V</u>	<u>S</u>	<u>F</u>	<u>W</u>	<u>I</u>	<u>N</u>	<u>M</u>	<u>D</u>	<u>A</u>	<u>A</u>	<u>P</u>	<u>A</u>	300			

Figure 2B

901	CGTGTGGGCCTGGGCATCACCAACCGTGCTCACCATGACCACCCAGAGCTCTGGCTCCGG	960
301	R <u>V</u> <u>G</u> <u>L</u> <u>G</u> <u>I</u> <u>T</u> <u>T</u> <u>V</u> <u>L</u> <u>T</u> <u>M</u> <u>T</u> <u>T</u> <u>Q</u> <u>S</u> <u>S</u> <u>G</u> <u>S</u> <u>R</u>	320
961	GCCTCTTGCCTAAGGTGTCCTACGTGAAGGCAATCGACATCTGGATGGCTGTGTCTG	1020
321	A <u>S</u> <u>L</u> <u>P</u> <u>K</u> <u>V</u> <u>S</u> <u>Y</u> <u>V</u> <u>K</u> <u>A</u> <u>I</u> <u>D</u> <u>I</u> <u>W</u> <u>M</u> <u>A</u> <u>V</u> <u>C</u> <u>L</u>	340
1021	CTCTTGTGTTCGCTGCCTGCTGGAGTATGCTGCCATAAATTGTTCTCGTCAGCAT	1080
341	<u>L</u> <u>F</u> <u>V</u> <u>F</u> <u>A</u> <u>A</u> <u>L</u> <u>L</u> <u>E</u> <u>Y</u> <u>A</u> <u>A</u> <u>I</u> <u>N</u> <u>F</u> <u>V</u> <u>S</u> <u>R</u> <u>Q</u> <u>H</u>	360
1081	AAAGAATTCAACGACTTCGAAGAAGGCAGAGGCAGGCCAACGCTTGGAGGAAGATATCATC	1140
361	K <u>E</u> <u>F</u> <u>I</u> <u>R</u> <u>L</u> <u>R</u> <u>R</u> <u>Q</u> <u>R</u> <u>R</u> <u>Q</u> <u>R</u> <u>L</u> <u>E</u> <u>E</u> <u>D</u> <u>I</u> <u>I</u>	380
1141	CAAGAAAGTCGTTCTATTCCGTGGCTATGGCTTGGCCACTGCCTGCAGGAAGAGAT	1200
381	Q <u>E</u> <u>S</u> <u>R</u> <u>F</u> <u>Y</u> <u>F</u> <u>R</u> <u>G</u> <u>Y</u> <u>G</u> <u>L</u> <u>G</u> <u>H</u> <u>C</u> <u>L</u> <u>Q</u> <u>A</u> <u>R</u> <u>D</u>	400
1201	GGAGGTCCAATGGAAGGTTCTGGCATTATAGTCCCCAACCTCCAGCCCCCTTTCTAAGG	1260
401	G <u>G</u> <u>P</u> <u>M</u> <u>E</u> <u>G</u> <u>S</u> <u>G</u> <u>I</u> <u>Y</u> <u>S</u> <u>P</u> <u>Q</u> <u>P</u> <u>P</u> <u>A</u> <u>P</u> <u>L</u> <u>L</u> <u>R</u>	420
1261	GAAGGAGAAACCACGCGGAAACTCTACGTGGACTGAGCCAAGAGAATTGACACCATCTCC	1320
421	E <u>G</u> <u>E</u> <u>T</u> <u>T</u> <u>R</u> <u>K</u> <u>L</u> <u>Y</u> <u>V</u> <u>D</u>	431
1321	CGGGCTGTCTCCCTTCACTTCCTCATCTCAATATCTTCTACTGGGTTGTCTATAAA	1380
1381	GTGCTATGGTCAGAAGATATCCACCAGGCTCTGTGAATAGGGTGGAGCTATAGAGTCCT	1440
1441	GCTGCTGGCCTCCTGCTCCTCCTGGTGGCTTCTCCCTCAGTTAGACTCCATTAGGG	1500
1501	GTGGACAGTTCCCTGATCTCCACTCAGAACTCAACTACCAGTCCAAAGCTAT	1560
1561	GTGGCCTATATTGCATGGTGCCAATGGTGGCTGTACTTATAAAGATGGCTTATCTACCC	1620
1621	TAAAAAAAAAAAAAAAAAAA 1640	

Figure 3A

		1	
GRA1_HUMAN	(1)	-----MYSFNTLRLYLSGAIVEFSLAASKEAEEAARSATKPMSPSDFLDK	
GRA3_HUMAN	(1)	-MAHVRHFRTLWVSGFYWEAALLSLVATKEFTDSARSRSAPMSPSDFLDK	
HGRA4	(1)	MTTLVPATLSFLLLWTLPGQVLLRVALAKEEVKSGIKGSQPMSPSDFLDK	
HGRA4sv	(1)	MTTLVPATLSFLLLWTLPGQVLLRVALAKEEVKSGIKGSQPMSPSDFLDK	
GRA4_MOUSE	(1)	-----VALAKEDVKSGLKGSQPMSPSDFLDK	
GRA2_HUMAN	(1)	MNRQIVNILTALEAFFLEETNHFRTAFCKDHDSSRGKOPSQTLSPSDFLDK	
		51	
GRA1_HUMAN	(45)	LMGRTSGYDARIRPNFKGPPVNVSCNIFINSFGSIAETTMDYRVNTFLRQ	
GRA3_HUMAN	(50)	LMGRTSGYDARIRPNFKGPPVNTCNIFINSFGSIAETTMDYRVNTFLRQ	
HGRA4	(51)	LMGRTSGYDARIRPNFKGPPVNTCNIFINSFGSIAETTMDYRVNTFLRQ	
HGRA4sv	(51)	LMGRTSGYDARIRPNFKGPPVNTCNIFINSFGSIAETTMDYRVNTFLRQ	
GRA4_MOUSE	(27)	LMGRTSGYDARIRPNFKGPPVNTCNIFINSFGSVTETTMDYRVNTFLRQ	
GRA2_HUMAN	(51)	LMGRTSGYDARIRPNFKGPPVNTCNIFINSFGSVTETTMDYRVNTFLRQ	
		101	
GRA1_HUMAN	(95)	QWNDPRLAYNEYPDDSLDLDPSMLDSIWKPDLFANEKGAHFHEVTTDNK	
GRA3_HUMAN	(100)	KWNDPRLAYS EYPDDSLDLDPSMLDSIWKPDLFANEKGANFHEVTTDNK	
HGRA4	(101)	QWNDPRLSYREYPDDSLDLDPSMLDSIWKPDLFANEKGANFHEVTTDNK	
HGRA4sv	(101)	QWNDPRLSYREYPDDSLDLDPSMLDSIWKPDLFANEKGANFHEVTTDNK	
GRA4_MOUSE	(77)	QWNDPRLAYREYPDDSLDLDPSMLDSIWKPDLFANEKGANFHEVTTDNK	
GRA2_HUMAN	(101)	QWNDSRLAYSEYPDDSLDLDPSMLDSIWKPDLFANEKGANFHDVTTDNK	
		151	
GRA1_HUMAN	(145)	LLRISRNGNVLYSIRTLTLACPMMDLKNFPMDVQTCIMQLES-----	
GRA3_HUMAN	(150)	LLRIFKNGNVLYSIRTLTLSCPMDLKNFPMDVQTCIMQLES-----	
HGRA4	(151)	LLRIFKNGNVLYSIRTLTLISCLMDLKNFPMDVQTCIMQLES-----	
HGRA4sv	(151)	LLRIFKNGNVLYSIRTLTLISCLMDLKNFPMDVQTCIMQLESSSILCSPL	
GRA4_MOUSE	(127)	LLRIFKNGNVLYSIRTLTLISCPMDLKNFPMDVQTCIMQLES-----	
GRA2_HUMAN	(151)	LLRISKNGKVLYSIRTLTLSCPMDLKNFPMDVQTCIMQLES-----	
		201	
GRA1_HUMAN	(187)	-----FGYTMNDLIFEWQEQGA-VQVADGLTLQFILKEEKDLRYCTKH	
GRA3_HUMAN	(192)	-----FGYTMNDLIFEWQDEAP-VQVAEGLTLQFILKEEKDLRYCTKH	
HGRA4	(193)	-----FGYTMNDLIFEWQLEDAPAVQVAEGLTLQFILRDEKDLGCCTKH	
HGRA4sv	(201)	PSLSSLGVGYTMNDLIFEWQLEDAPAVQVAEGLTLQFILRDEKDLGCCTKH	
GRA4_MOUSE	(169)	-----FGYTMNDLIFEWQLEDAPAVQVAEGLTLQFILRDEKDLGYCTKH	
GRA2_HUMAN	(193)	-----FGYTMNDLIFEWLSDGP-VQVAEGLTLQFILKEEKELGYCTKH	
		251	[<<<<<<<TM1>>>>>>>>]
GRA1_HUMAN	(230)	YNTGKFTCIEARFHRLERQMGYYLIQMYIPSLILIVLSWVSFWINMDAAPA	300
GRA3_HUMAN	(235)	YNTGKFTCIEVRFHRLERQMGYYLIQMYIPSLILIVLSWVSFWINMDAAPA	
HGRA4	(237)	YNTGKFTCIEVKFHRLERQMGYYLIQMYIPSLILIVLSWVSFWINMDAAPA	
HGRA4sv	(251)	YNTGKFTCIEVKFHRLERQMGYYLIQMYIPSLILIVLSWVSFWINMDAAPA	
GRA4_MOUSE	(213)	YNTGKFTCIEVKFHRLERQMGYYLIQMYIPSLILIVLSWVSFWINMDAAPA	
GRA2_HUMAN	(236)	YNTGKFTCIEVKFHRLERQMGYYLIQMYIPSLILIVLSWVSFWINMDAAPA	
		3 [<<<<<<TM2>>>>]	[<<<<<<<TM3
GRA1_HUMAN	(280)	RVGLGITVLTMTTQSSGRASLPKVSYVKAIDIWMAVCLLFVFSALLEY	
GRA3_HUMAN	(285)	RVALGITVLTMTTQSSGRASLPKVSYVKAIDIWMAVCLLFVFSALLEY	
HGRA4	(287)	RVGLGITVLTMTTQSSGRASLPKVSYVKAIDIWMAVCLLFVFAALLEY	
HGRA4sv	(301)	RVGLGITVLTMTTQSSGRASLPKVSYVKAIDIWMAVCLLFVFAALLEY	
GRA4_MOUSE	(263)	RVGLGITVLTMTTQSSGRASLPKVSYVKAIDIWMAVCLLFVFAALLEY	
GRA2_HUMAN	(286)	RVALGITVLTMTTQSSGRASLPKVSYVKAIDIWMAVCLLFVFAALLEY	

**Figure 3B**

		>>>>>]		
GRA1_HUMAN	(330)	AAVNFVSRQHKELLRERRKRR-----	HHKEDEAGEGRFNFS	400
GRA3_HUMAN	(335)	AAVNFVSRQHKELLRERRKRKNKTEAFALEKFYRFSDMDDDEVRESRFSFT		
HGRA4	(337)	AAVNFVSRQHKEFTRLRRRQR-----	RQRQEEDEHQESRFYFR	
HGRA4sv	(351)	AAVNFVSRQHKEFTRLRRRQR-----	RQRQEEDEHQESRFYFR	
GRA4_MOUSE	(313)	AAVNFVSRQXKEFMRLLRRRQR-----	RQRM	
GRA2_HUMAN	(336)	AAVNFVSRQHKEFRLRRLRQR-----	RQNKKEEDWIRESRFNFS	
		401		450
GRA1_HUMAN	(366)	AYGMGPACLQAKDGISVKGANNSTTNPPPPAPS <span style="background-color: black; color: black;">KS</span> PEEYRKLF <span style="background-color: black; color: black;">IQ</span> RAKKI		
GRA3_HUMAN	(385)	AYGMGP-CLQAKDGMTPKGPN-----HPVQVMPKSPD <span style="background-color: black; color: black;">EM</span> RKV <span style="background-color: black; color: black;">F</span> DRAKKI		
HGRA4	(375)	GYGMGH-CLQAKDG <span style="background-color: black; color: black;">AD</span> GGPM <span style="background-color: black; color: black;">EGS</span> -GIY <span style="background-color: black; color: black;">S</span> PQPPAP <span style="background-color: black; color: black;">IL</span> REGETTRKL <span style="background-color: black; color: black;">V</span> D-----		
HGRA4sv	(389)	GYGMGH-CLQAKDG <span style="background-color: black; color: black;">AD</span> GGPM <span style="background-color: black; color: black;">EGS</span> -GIY <span style="background-color: black; color: black;">S</span> PQPPAP <span style="background-color: black; color: black;">IL</span> REGETTRKL <span style="background-color: black; color: black;">V</span> D-----		
GRA4_MOUSE	(338)	-----		
GRA2_HUMAN	(374)	GYGMGH-CLQAKDGTA <span style="background-color: black; color: black;">V</span> KATPANPLPQPPP-----D <span style="background-color: black; color: black;">G</span> CDA <span style="background-color: black; color: black;">KKK</span> FVDRAK <span style="background-color: black; color: black;">R</span> I		
		451		487
GRA1_HUMAN	(416)	DKISRIGFP <span style="background-color: black; color: black;">MA</span> FLIFN <span style="background-color: black; color: black;">MF</span> YW <span style="background-color: black; color: black;">I</span> Y <span style="background-color: black; color: black;">Y</span> KI <span style="background-color: black; color: black;">V</span> R <span style="background-color: black; color: black;">R</span> ED <span style="background-color: black; color: black;">D</span> MHNQ-----		
GRA3_HUMAN	(429)	DTISRACFPT <span style="background-color: black; color: black;">IA</span> FLIFN <span style="background-color: black; color: black;">MF</span> YW <span style="background-color: black; color: black;">V</span> Y <span style="background-color: black; color: black;">Y</span> KI <span style="background-color: black; color: black;">V</span> R <span style="background-color: black; color: black;">H</span> ED <span style="background-color: black; color: black;">D</span> HHQQOD		
HGRA4	(418)	-----		
HGRA4sv	(432)	-----		
GRA4_MOUSE	(338)	-----		
GRA2_HUMAN	(419)	DTISRRAAFPT <span style="background-color: black; color: black;">IA</span> FLIFN <span style="background-color: black; color: black;">MF</span> YW <span style="background-color: black; color: black;">I</span> Y <span style="background-color: black; color: black;">Y</span> KI <span style="background-color: black; color: black;">V</span> R <span style="background-color: black; color: black;">H</span> ED <span style="background-color: black; color: black;">D</span> HKK-----		

卷之三

Figure 4

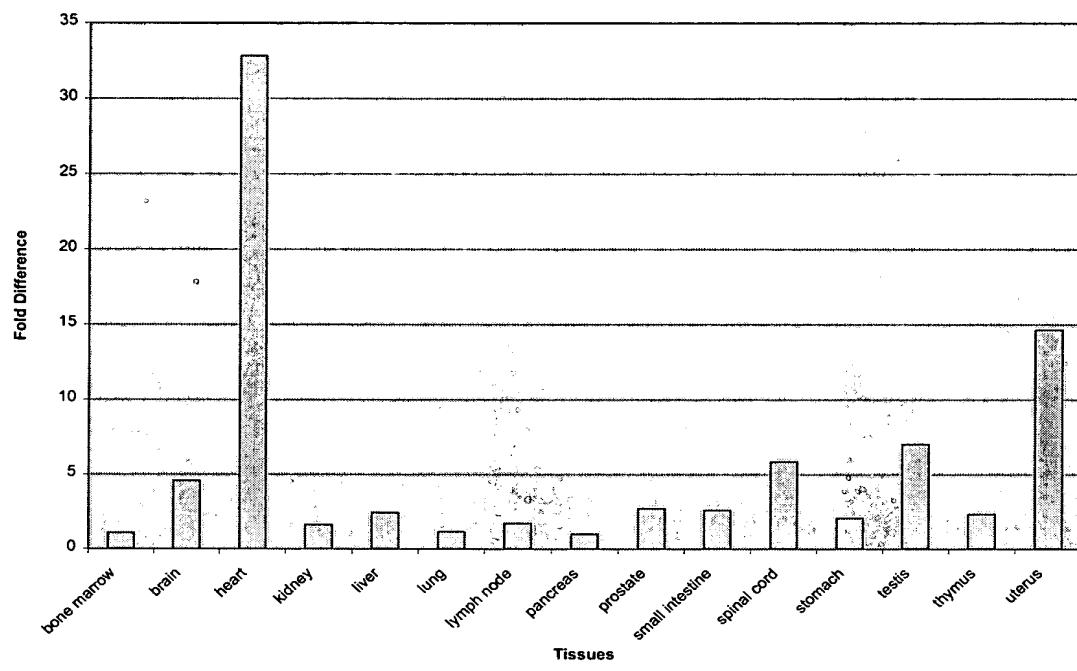


Figure 5

G1934909\_001 MTTLVPATLSFLLLWTLPGQVLLRVALAKEEVKGSGTGSQPMSPSDFLDKLMGRSGYDA  
 cloneE3 MTTLVPATLSFLLLWTLPGQVLLRVALAKEEVKGSGTGSQPMSPSDFLDKLMGRSGYDA  
 cloneD8 MTTLVPATLSFLLLWTLPGQVLLRVALAKEEVKGSGTGSQPMSPSDFLDKLMGRSGYDA  
 \*\*\*\*\*

G1934909\_001 RIRPNFKGPPVNVTCNIFINSFSSITKTTMACWAPGNGNVSEGPIAPSQDYRVNVFLRQ  
 cloneE3 RIRPNFKGPPVNVTCNIFINSFSSVTKTTM-----DYRVNVFLRQ  
 cloneD8 RIRPNFKGPPVNVTCNIFINSFSSVTKTTM-----DYRVNVFLRQ  
 \*\*\*\*\*:\*\*\*\*\* : : . . :\*\*\*\*\*

G1934909\_001 QWNDPLRSYREYPDDSLDDPSMLDSIWKPDLFFANEGKANFHEVTTDNKLLRIFKNGNV  
 cloneE3 QWNDPLRSYREYPDDSLDDPSMLDSIWKPDLFFANEGKANFHEVTTDNKLLRIFKNGNV  
 cloneD8 QWNDPLRSYREYPDDSLDDPSMLDSIWKPDLFFANEGKANFHEVTTDNKLLRIFKNGNV  
 \*\*\*\*\*

G1934909\_001 LYSIRLTLILSCLMDLKNFPMIDIQTCTMQLES-----FGYTMKDLVFEWLE  
 cloneE3 LYSIRLTLILSCLMDLKNFPMIDIQTCTMQLES-----FGYTMKDLVFEWLE  
 cloneD8 LYSIRLTLILSCLMDLKNFPMIDIQTCTMQLES-----FGYTMKDLVFEWLE  
 \*\*\*\*\*

G1934909\_001 DAPAVQVAEGLTLPQFILRDEKDLGCCTKHNTGKFTCIEVKFHLEHQMGYYLIQMYIPS  
 cloneE3 DAPAVQVAEGLTLPQFILRDEKDLGCCTKHNTGKFTCIEVKFHLEHQMGYYLIQMYIPS  
 cloneD8 DAPAVQVAEGLTLPQFILRDEKDLGCCTKHNTGKFTCIEVKFHLEHQMGYYLIQMYIPS  
 \*\*\*\*\*

G1934909\_001 LLIVILSWVSFWINMDAAPARVGLGITTVLTMTTQSSGSRASLPK-----  
 cloneE3 LLIVILSWVSFWINMDAAPARVGLGITTVLTMTTQSSGSRASLPKVSYVKAIDIWMAVCL  
 cloneD8 LLIVILSWVSFWINMDAAPARVGLGITTVLTMTTQSSGSRASLPKVSYVKAIDIWMAVCL  
 \*\*\*\*\*

G1934909\_001 -----  
 cloneE3 LFVFAALLEYAAINFVSRQHKEFIRLRRQRQRLEEDIIQESRFYFRGYGLGHCLQARD  
 cloneD8 LFVFAALLEYAAINFVSRQHKEFIRLRRQRQRLEEDIIQESRFYFRGYGLGHCLQARD

G1934909\_001 -----  
 cloneE3 GGPMEGSGIYSPQPPAPLLREGETTRKLYVD  
 cloneD8 GGPMEGSGIYSPQPPAPLLREGETTRKLYVD

14  
 13  
 12  
 11  
 10  
 9  
 8  
 7  
 6  
 5  
 4  
 3  
 2  
 1

Figure 6.

**HGRA4**

<u>Protein</u>	<u>Genbank ID</u>	<u>Identities</u>	<u>Similarities</u>
human glycine receptor alpha-1 subunit	gi 4504019	76.8%	82.2%
human glycine receptor alpha 3 subunit	gi 5729844	84.4%	78.7%
mouse glycine receptor subunit alpha 4 protein	gi 817957	97%	96%
human glycine receptor alpha 2 subunit	gi 4504021	80.6%	86.5%

**HGRA4sv**

<u>Protein</u>	<u>Genbank ID</u>	<u>Identities</u>	<u>Similarities</u>
human glycine receptor alpha-1 subunit	gi 4504019	76.5%	82%
human glycine receptor alpha 3 subunit	gi 5729844	78.5%	84.2%
mouse glycine receptor subunit alpha 4 protein	gi 817957	95.8%	96.7%
human glycine receptor alpha 2 subunit	gi 4504021	80.3%	86.2%

**Figure 7**

**Atgacaactttgttctgcaccccttccttccttcgtggaccctgcagggcaggccctcagggtggcct**  
**tggcaaaagaggaagtcaaatcttgcaccaagggtccagccatgtccccctctgatttcttagacaaacttatggg**  
**gcgaacatctggatatgtgcgcaggattcgcccaatttaaggcccacccgtgaacgtgacccgcacatcttcatc**  
**aacagttcagctccatccaagaccacaatggctgtggccctggaaatggcaatgtttctgaaggggccatata**  
**ctgcacccctccaggactaccgggtgaatgtcttcttgcggcaacagtgaaatgaccacgcctgtcctaccgagaata**  
**tcctgtatgactcttgacccatcgatccctccatgtggactctatcttgcggacccgcacatcttcttgcataatgaaaa**  
**ggggcaacttccatgggtgaccacggacaacaagttactgcgcacatcttcaagaatggaaatgtgtacagcatca**  
**ggctgaccctcatttgcctgcgtatggaccccaagaacttccatggacatccagacactgcacgatgcagctga**  
**gagcttgcgtacaccatgaaagacctcggtttgagttggctggaaatgtctgttgccttgcgtggctgagggctg**  
**actctgcccagttatcttgcggatgagaaggatctaggctgttgcataaccacacaggaaattcacct**  
**gcatcgaggtaaagttcacctgaaacggcagatggctactatcttgcgttgcacatccccagccactcatgt**  
**catcctgtcctgggtctccttcgtcaacatggatgtctgccttgcgtggcatcaccaccgtgctc**  
**accatgaccacccagagctggcccccggctttgcctaag (SEQ ID NO:9)**

**Figure 8**

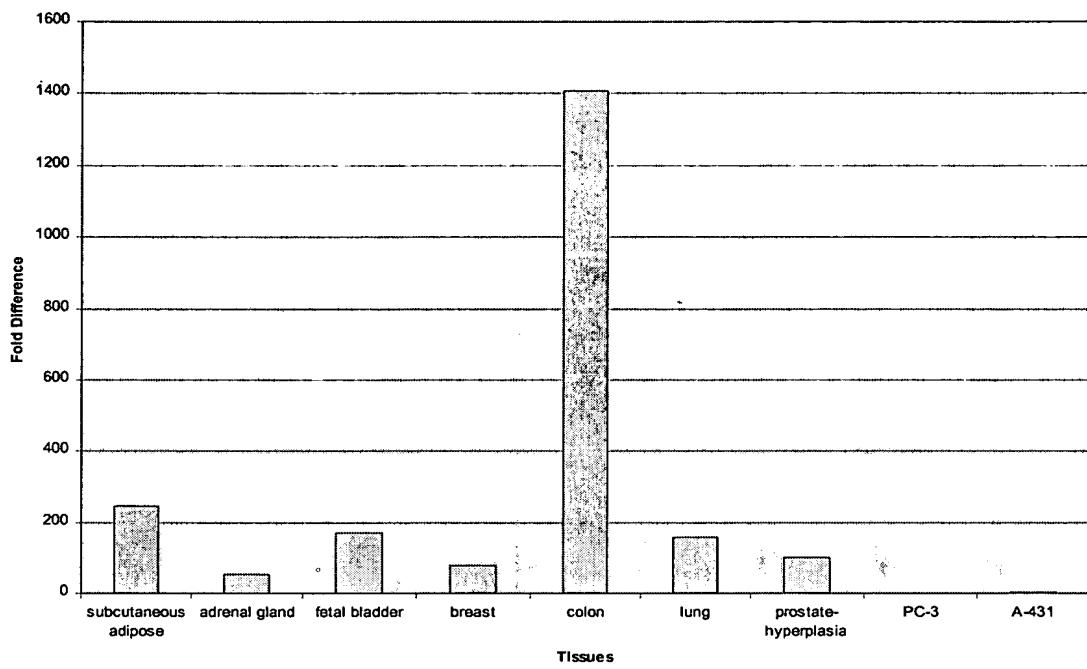


Figure 9

